

1 CACGCGTCCGCCACGCGTCCGGTGAGACAGAGGCAAAACAAAGGTGCTGAAAGCCAGAC 60  
-----+-----+-----+-----+-----+-----+  
GTGCGCAGGCGGGTGCGCAGGCCACTCTGTCTCCGTTTTGTTCCAGACTTTCGGTCTG

a H A S A H A S G E T E A K Q R C \* K P D -

61 ATGGAGTCAGAGATGAGTGATCCTCAGCCATTGCAGGAGGAAAGATATGATATGTCAGGT 120  
-----+-----+-----+-----+-----+-----+  
TACCTCAGTCTCTACTCACTAGGAGTCGGTAACGTCTCTTTCTATACTATACAGTCCA

a M E S E M S D P Q P L Q E E R Y D M S G -

121 GCCCGCCTGGCCCTGACGCTGTGTGTCCACAAAGCCCGGGAGGGTTCGAGGTAgACATG 180  
-----+-----+-----+-----+-----+-----+  
CGGGCGGACCGGGACTGCGACACACAGTGGTTTCGGGCCCTCCAAGGCTCCATcTGTAC

a A R L A L T L C V T K A R E G S E V D M -

181 GAGGCCCTGGAACGCATGTTCCGTTACCTGAAATTTGAAAGCACCATGAAGAGGGATCCC 240  
-----+-----+-----+-----+-----+-----+  
CTCCGGGACCTTGCGTACAAGGCAATGGACTTTAACTTTCGTGGTACTTCTCCCTAGGG

a E A L E R M F R Y L K F E S T M K R D P -

241 ACCGCCAGCAATTTCTGGAAGAGTTGGATGAATTTGAGCAGACCATAGATAATTGGGAA 300  
-----+-----+-----+-----+-----+-----+  
TGCGGGTTCGTTAAAGACCTTCTCAACCTACTTAAAGTCGTCTGGTATCTATTAACCTT

a T A Q Q F L E E L D E F Q Q T I D N W E -

301 GAGCCTGTCAGCTGTGCCTTTGTGGTACTCATGGCACATGGTGAGGAAGGCCTCCTCAAG 360  
-----+-----+-----+-----+-----+-----+  
CTCGGACAGTCGACACGGAAACACCATGAGTACCGTGTACCACTCCTTCGGAGGAGTTC

a E P V S C A F V V L M A H G E E G L L K -

361 GGAGAAGATGAGAAGATGGTCAGACTAGAAGACCTTTTTGAAGTCTTGAACAACAAGAAC 420  
-----+-----+-----+-----+-----+-----+  
CCTCTTCTACTCTTCTACCAGTCTGATCTTCTGGAAAACTTCAGAACTTGTTGTTCTTG

a G E D E K M V R L E D L F E V L N N K N -

421 TGCAAGGCCCTGAGAGGCAAGCCAAAGGTGTACATCATCCAGGCTTGTAGAGGAGAGCAC 480  
-----+-----+-----+-----+-----+-----+  
ACGTTCCGGGACTCTCCGTTCCGTTTCCACATGTAGTAGGTCCGAACATCTCCTCTCGTG

*Fig. 1A*

a C K A L R G K P K V Y I I Q A C R G E H -  
AGAGACCCCGGTGAGGAACTACGTGGAAATGAGGAACTAGGTGGAGATGAGGAACTNGGT  
481 -----+-----+-----+-----+-----+-----+ 540  
TCTCTGGGGCCACTCCTTGATGCACCTTTACTCCTTGATCCACCTCTACTCCTTGANCCA

a R D P G E E L R G N E E L G G D E E L G -  
GGAGATGAGGTTGCTGTGCTCAAGAACAACCCCCAAAGTATCCCAACCTATACGGATACC  
541 -----+-----+-----+-----+-----+-----+ 600  
CCTCTACTCCAACGACACGAGTTCTTGTTGGGGGTTTCATAGGGTTGGATATGCCTATGG

a G D E V A V L K N N P Q S I P T Y T D T -  
CTCCACATCTACTCCACGGTAGAGGGGTACCTCTCCTATAGACATGACGAGAAAGGCTCT  
601 -----+-----+-----+-----+-----+-----+ 660  
GAGGTGTAGATGAGGTGCCATCTCCCCATGGAGAGGATATCTGTACTGCTCTTTCCGAGA

a L H I Y S T V E G Y L S Y R H D E K G S -  
GGCTTCATCCAGACCCTGACGGATGTGTTTCATTCATAAAAAAGGATCCATCTTAGAACTG  
661 -----+-----+-----+-----+-----+-----+ 720  
CCGAAGTAGGTCTGGGACTGCCTACACAAGTAAGTATTTTTCTAGGTAGAATCTTGAC

a G F I Q T L T D V F I H K K G S I L E L -  
ACAGAAGAGATCACCCGACTTATGGCAAACACGGAGGTGATGCAGGAAGGAAAACCAAGG  
721 -----+-----+-----+-----+-----+-----+ 780  
TGTCTTCTCTAGTGGGCTGAATACCGTTTGTGCCTCCACTACGTCTTCCTTTTGGTTCC

a T E E I T R L M A N T E V M Q E G K P R -  
AAAGTGAACCCTGAAGTCCAAAGCACCCCTCCGGAAGAAGCTCTATTTGCAATAAAAGAGA  
781 -----+-----+-----+-----+-----+-----+ 840  
TTTCACTTGGGACTTCAGGTTTCGTGGGAGGCCTTCTTCGAGATAAACGTTATTTTCTCT

a K V N P E V Q S T L R K K L Y L Q \* K R -  
GGGCAGGGAT  
841 -----+ 850  
CCCGTCCCTA

a G Q G -

*Fig. 1B*

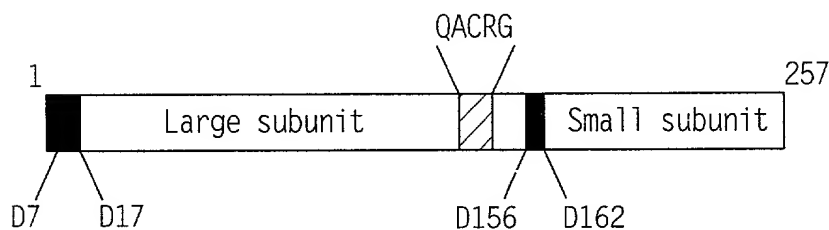
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casp-12	-----MAARRTHERDPIYKIKGLAKDMLDGV	26
casp-1	-----MADKILRAKRQFINSVSIGTINGL	25
casp-3	-----	
casp-7	-----	
casp-6	-----	
casp-8	MDFQSCDAIAEELGSEDLAALKFLCLDYIPHKLETIEDAQLFLRLREKGMLEENLSFLKELLFHISRWDLLVNFDCNREEMVRELDRDPRQCPRL	100
casp-2	-----MAAPSGRSQSSLHRKGLMAADRRSRLAVCGMHPDHQETLKKNRVVLAKQLL	52
casp-14	-----	
casp-11	-----MAENKHPDKPLKVLEQLGKEVL..TEYLEKLVSQSNVLKLEEDKQKFNNNAERSDKRWV.FV.DAMKKKHSGKVGEMLLQTFFSVDPG	82
casp-12	FDDLVEKNVLNGDELLKIGESASFLNKAENLVENFLEKTMAGKIFAGHIANSEQQLSLQFSDNEDDGPOKICTPSSPSESRRKVEDDEMEVNLAGE	126
casp-1	LDELLEKRVLNQEEMDKIKLANITAMDKARDLCOHVSCKGPQASQIFITYICNEDCYLAGILELQSAETAFTVATEDSKGGHPSSSETKEEQN..KEDG	123
casp-3	-----MENNKTSV	8
casp-7	-----MTDDQDCAAELEKVDSSSEDGVDAPDRSSI	31
casp-6	-----	
casp-8	PYRSCSFRLSEEVSLELRSFKLLNNEIPCKLEDDLILLEIFVEMEKRTMLAENNELTKSICDQVNSLLGKIEDYERSSTERRMSLEGREELPPSV	200
casp-2	LSLELHLLLEKDIITLEMRELIAKGGFSQNVLLNLLPKRGPAFADFCEALRETRQGHLEDLLLTSLDIQHVLPPLSCDYDTSLPFSVCESCPPHK	152
casp-14	-----	
casp-11	SHHGAEANLEMEPEESLNTLKLCSPEEFTRLCREKTQEIYPIKEAN.GRTRKALIICTEFKHLRLRYGANFDIIGMKGLLEDLGYDVVVKELTAEGME	181
casp-12	SHMLTAPHGLQSSEVQDTLKLCPDQFCIKTERAKEIYPVMEKE.GRTRLALII CNKFDYLFDRDNADTDILNMQELLENLGYSVVLKENLTAQEME	225
casp-1	TFPGLTG.....TLKFCPLEKAQKLWKENPSEIYIMNTT.TRTRLALIICTEFQHLSPRVGAQVDLREMKLLLEDLGYTVKVKENLTALEMV	211
casp-3	DSKSINWFVKTIHGSKSVDSGIYLDSSYKMDYPEMGIICIIINNKNFHKS.....TGMSSRSGTDVDAANLRETFMGLKYCVRNKNDLTREDIL	97
casp-7	ISSILLKKRNASAGPVRTGRDVPYLYRMDFOKMGKCIINNKNFDKA.....TGMVVRNGTDKAGALFKCFQNLGFVTVHNDSCAKMQ	120
casp-6	-----MTETDGYKSRVFDPAEQYKMDHKRRGVALIFNHERFFWH.....LTLPERRGTNADRNLTTRFSDLGFEVKCFNDLRAEELL	80
casp-8	LDEMSLKMAELCDSPREQDESRTSDKVYQMKNKPRGYCLII NNHDFSKA...REDITQLRKMMDRKGTDCKEALSKTFKELHFEIVSYDDCTANEIH	296
casp-2	QLRLSTDATEHSLDNGDPPCLLVKPCPTEFYQAHYQLAYRLQSQPRGLALVLSNVHFTGEKDLFRSGGDVDHTTLVTLFKLLGYNVHVLHDQTAQEMQ	252
casp-14	-----MESEMSDQPLQEERYDMSGARLALTL CVTK...AREGSEVDMEALERMFRYLKFESTMKRDPATAQQL	66
casp-11	SEMDKFAAL..SEHQTSDSSTFLVMSHGTLHGICGTMHSEKTPDVLQYDTIYQIFNNCHCPGLRDKPKVII IQACRGNGSGEMMIRESSKPQLCRGVDP	279
casp-12	TELMQFAGR..PEHQSSDSSTFLVMSHGILEGICGVKHRNKKPDVLHDDTIFKIFNNSNCRSLRNKPKILIMQACRGRYNGTIWV.STNKGIATADTDEE	322
casp-1	KEVKEFAAC..PEHKTSDSSTFLVMSHGIEGICGTTYSNEVSDILKVDITFQMMNTLKCPSLKDKPKVII IQACRGEKQGVLLKDS....VRDSEED	304
casp-3	ELMDSVSK...EDHSKRSSFVCVILSHGDEGVYGTNGP.....VELKKLSFFRGDYCRSLTGKPKLFI IQACRGTELDGCI.....ETDS...G	177
casp-7	DLLRKASE...EDHSNSACFACVLLSHGEEDLIYKGDGV.....TPIKDLTAHFRGDRCKTLLEKPKLFI IQACRGTELDGCI.....QADS...G	200
casp-6	LKIHVEST...SSHIDADCFCVFLSHGEGNHVYAYDAK....TEIQTLTGLFKGDKQSLVGKPKIFI IQACRGSQHDVVPVPLDMVDHQTDK..LD	169
casp-8	EILEGYQS...ADHKNKDCFCICILSHGDKGVVYGTGK....EASIDYLTSTYFTGSKCPSLSGKPKIFFI IQACRGSNFQKGVPEAGFEQNH...LE	356
casp-2	EKLQNFQA.LPAHRVTSVC.VALLSHGVEGGIYGVGDK....LLQLQEVFRLFDNANCPSLQNKPKMFFI IQACRGDETDRGVDQDQGNHTQSPGCEE	345
casp-14	EELDEFQQTIDNWEPEVSCAFVLLMHGEEGLLGEDEK....MVRLEDLFEVLNNKNCKALRGKPKVYI IQACRGHEHDPGEELRGNEELGGDEELGG	161

Fig. 2A-1

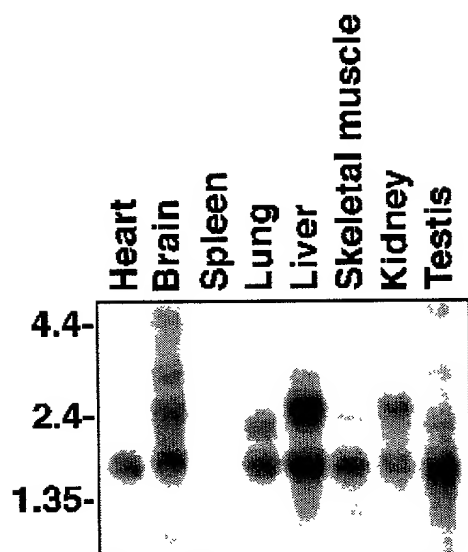
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 casp-12 RVLSCKW.NNSITKAHVETDFIAFKSSTPHNISWRVGKTSLSFISKLIDCFKKYCWCYHLEEIFRKVQHSFEVPGELTQMPTIERVSMTRYFYFLFPGN-- 419  
 casp-1 FLTDAIFEDDGIMKAHIEKDFIAFCSSTPDNVSWRHPVRGSLFIESLIKMKKEYAWSCDLEIFRKVRFSFEQPEFRLQMPTADRVTLTKRFYFLFPGH-- 402  
 casp-3 ..TDEEMAC...QKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCSMLKLY..AHKLEFMHILTRVNRKVATEFESFSLDSTFHAKKQIPCIVSMLT 270  
 casp-7 ..PINDIDANPRNKIPVEADFLFAYSTVPGYYSWRNPGKGSWFQALCSILNEH..GKDLEIMQILTRVNDVARHFESQSDPRFNEKKQIPCMVSMLT 296  
 casp-6 ..NVTQVDAASYTLPAAGDFLMCYSVAEGYYSHRETVNGSWYIQDLCEMLARY..GSSLEFTELLTLVNRKVSQRRVDFCKDPAIGKKQVPCFASMLT 265  
 casp-8 ..VDS...SSHKNYIPDEADFLGMATVLMCVSYRDPVNGTWYIQSLCQSLRERC.PQDDILSILTGVNYDVS.....KDDRRNKGGKMPQPTFTLR 474  
 casp-2 ..SDAGKEELMKMRLPTRSDMICGYACLKGNAAMRNTKRGSWYIEALTQVFSERA.C.DMHVADMLVKVNALIKER.EGYAPGTEFHRCKEMSEYCSLTC 440  
 casp-14 ..DEAVLKNPQSIPTYTDTLHIYSTVEGYLSYRHDEKSGFIQTLDVFIHKK.G.S..ILELTEEITRLMANT.EVMQEGKP...RKVNPEVQSTLR 251

casp-11 -----  
 casp-12 -----  
 casp-1 -----  
 casp-3 KELYFYH----- 277  
 casp-7 KELYFSR----- 303  
 casp-6 KKLHFCPKPSK- 276  
 casp-8 KKL----- 477  
 casp-2 QQLYLFPGYPPT 452  
 casp-14 KKLYLQ----- 257

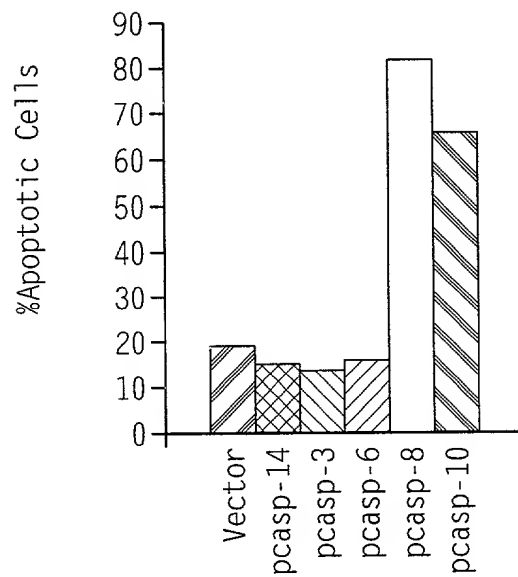
*Fig. 2A-2*



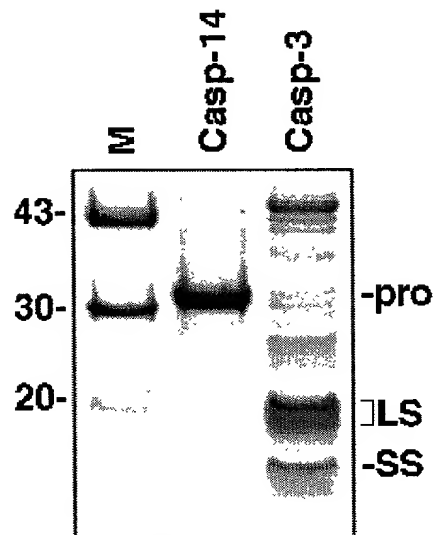
*Fig. 2B*



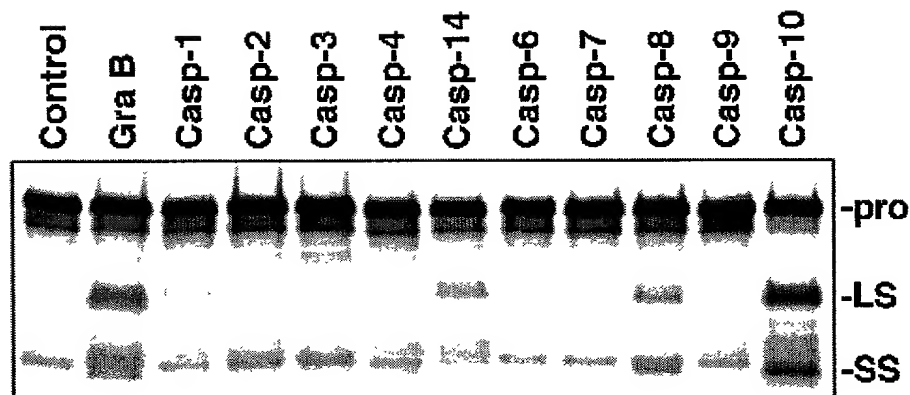
*Fig. 3*



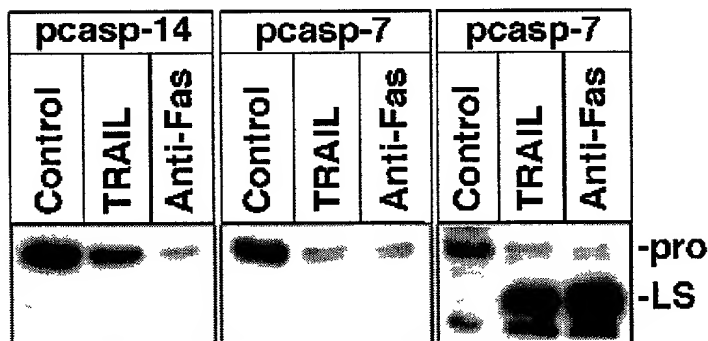
*Fig. 4*



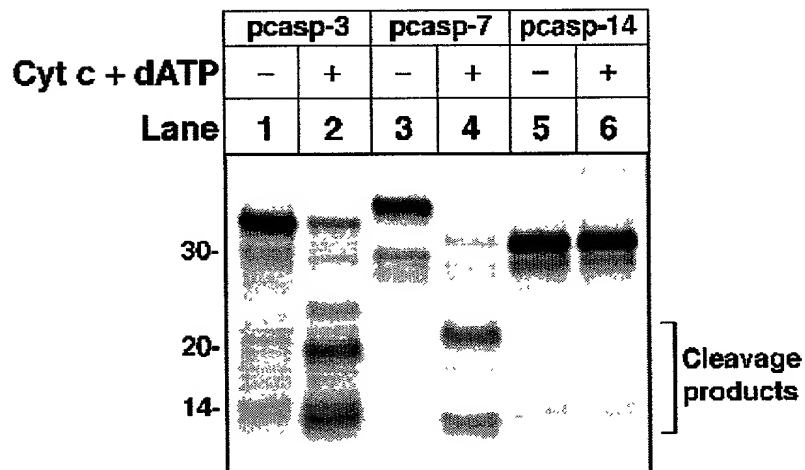
*Fig. 5A*



*Fig. 5B*



*Fig. 5C*



*Fig. 6*



```

aggatcagac aagggtgctg agagccggga ctcacaacca aaggagaa atg agc aat 57
                                         Met Ser Asn
                                         1

ccg cgg tct ttg gaa gag gag aaa tat gat atg tca ggt gcc cgc ctg 105
Pro Arg Ser Leu Glu Glu Glu Lys Tyr Asp Met Ser Gly Ala Arg Leu
      5              10              15

gcc cta ata ctg tgt gtc acc aaa gcc cgg gaa ggt tcc gaa gaa gac 153
Ala Leu Ile Leu Cys Val Thr Lys Ala Arg Glu Gly Ser Glu Glu Asp
    20              25              30              35

ctg gat gct ctg gaa cac atg ttt cgg cag ctg aga ttc gaa agc acc 201
Leu Asp Ala Leu Glu His Met Phe Arg Gln Leu Arg Phe Glu Ser Thr
              40              45              50

atg aaa aga gac ccc act gcc gag caa ttc cag gaa gag ctg gaa aaa 249
Met Lys Arg Asp Pro Thr Ala Glu Gln Phe Gln Glu Glu Leu Glu Lys
              55              60              65

ttc cag cag gcc atc gat tcc cgg gaa gat ccc gtc agt tgt gcc ttc 297
Phe Gln Gln Ala Ile Asp Ser Arg Glu Asp Pro Val Ser Cys Ala Phe
      70              75              80

gtg gta ctc atg gct cac ggg agg gaa ggc ttc ctc aag gga gaa gat 345
Val Val Leu Met Ala His Gly Arg Glu Gly Phe Leu Lys Gly Glu Asp
    85              90              95

ggg gag atg gtc aag ctg gag aat ctc ttc gag gcc ctg aac aac aag 393
Gly Glu Met Val Lys Leu Glu Asn Leu Phe Glu Ala Leu Asn Asn Lys
    100              105              110              115

aac tgc cag gcc ctg cga gct aag ccc aag gtg tac atc ata cag gcc 441
Asn Cys Gln Ala Leu Arg Ala Lys Pro Lys Val Tyr Ile Ile Gln Ala
              120              125              130

tgt cga gga gaa caa agg gac ccc ggt gaa aca gta ggt gga gat gag 489
Cys Arg Gly Glu Gln Arg Asp Pro Gly Glu Thr Val Gly Gly Asp Glu
      135              140              145

att gtg atg gtc atc aaa gac agc cca caa acc atc cca aca tac aca 537
Ile Val Met Val Ile Lys Asp Ser Pro Gln Thr Ile Pro Thr Tyr Thr
      150              155              160
    
```

*Fig. 7A*

gat gcc ttg cac gtt tat tcc acg gta gag gga tac atc gcc tac cga 585  
Asp Ala Leu His Val Tyr Ser Thr Val Glu Gly Tyr Ile Ala Tyr Arg  
165 170 175

cat gat cag aaa ggc tca tgc ttt atc cag acc ctg gtg gat gtg ttc 633  
His Asp Gln Lys Gly Ser Cys Phe Ile Gln Thr Leu Val Asp Val Phe  
180 185 190 195

acg aag agg aaa gga cat atc ttg gaa ctt ctg aca gag gtg acc cgg 681  
Thr Lys Arg Lys Gly His Ile Leu Glu Leu Leu Thr Glu Val Thr Arg  
200 205 210

cgg atg gca gaa gca gag ctg gtt caa gaa gga aaa gca agg aaa acg 729  
Arg Met Ala Glu Ala Glu Leu Val Gln Glu Gly Lys Ala Arg Lys Thr  
215 220 225

aac cct gaa atc caa agc acc ctc cgg aaa cgg ctg tat ctg cag tag 777  
Asn Pro Glu Ile Gln Ser Thr Leu Arg Lys Arg Leu Tyr Leu Gln  
230 235 240

*Fig. 7B*

```

aggatcagac aaggggtgctg agagccggga ctcaacaacca aaggagaa atg agc aat 57
                                     Met Ser Asn
                                     1

ccg cgg tct ttg gaa gag gag aaa tat gat atg tca ggt gcc cgc ctg 105
Pro Arg Ser Leu Glu Glu Glu Lys Tyr Asp Met Ser Gly Ala Arg Leu
      5              10              15

gcc cta ata ctg tgt gtc acc aaa gcc cgg gaa ggt tcc gaa gaa gac 153
Ala Leu Ile Leu Cys Val Thr Lys Ala Arg Glu Gly Ser Glu Glu Asp
    20              25              30              35

ctg gat gct ctg gaa cac atg ttt cgg cag ctg aga ttc gaa agc acc 201
Leu Asp Ala Leu Glu His Met Phe Arg Gln Leu Arg Phe Glu Ser Thr
      40              45              50

atg aaa aga gac ccc act gcc gag caa ttc cag gaa gag ctg gaa aaa 249
Met Lys Arg Asp Pro Thr Ala Glu Gln Phe Gln Glu Glu Leu Glu Lys
      55              60              65

ttc cag cag gcc atc gat tcc cgg gaa gat ccc gtc agt tgt gcc ttc 297
Phe Gln Gln Ala Ile Asp Ser Arg Glu Asp Pro Val Ser Cys Ala Phe
      70              75              80

gtg gta ctc atg gct cac ggg agg gaa ggc ttc ctc aag gga gaa gat 345
Val Val Leu Met Ala His Gly Arg Glu Gly Phe Leu Lys Gly Glu Asp
      85              90              95

ggg gag atg gtc aag ctg gag aat ctc ttc gag gcc ctg aac aac aag 393
Gly Glu Met Val Lys Leu Glu Asn Leu Phe Glu Ala Leu Asn Asn Lys
    100              105              110              115

aac tgc cag gcc ctg cga gct aag ccc aag gtg tac atc ata cag gcc 441
Asn Cys Gln Ala Leu Arg Ala Lys Pro Lys Val Tyr Ile Ile Gln Ala
      120              125              130

tgt cga gga gaa caa agg gac ccc ggt gaa aca gta ggt gga gat gag 489
Cys Arg Gly Glu Gln Arg Asp Pro Gly Glu Thr Val Gly Gly Asp Glu
      135              140              145

att gtg atg gtc atc aaa gac agc cca caa acc atc cca aca tac aca 537
Ile Val Met Val Ile Lys Asp Ser Pro Gln Thr Ile Pro Thr Tyr Thr
      150              155              160
    
```

*Fig. 8A*

```

gat gcc ttg cac gtt tat tcc acg gta gag gga ccc acg ccc ttc cag 585
Asp Ala Leu His Val Tyr Ser Thr Val Glu Gly Pro Thr Pro Phe Gln
    165                170                175

gat ccc ctc tac cta ccc tct gaa gct ccc ccg aac cca cct ctc tgg 633
Asp Pro Leu Tyr Leu Pro Ser Glu Ala Pro Pro Asn Pro Pro Leu Trp
180                185                190                195

aat tcc cag gat aca tcg cct acc gac atg atc aga aag gct cat gct 681
Asn Ser Gln Asp Thr Ser Pro Thr Asp Met Ile Arg Lys Ala His Ala
                200                205                210

tta tcc aga ccc tgg tgg atg tgt tca cga aga gga aag gac ata tct 729
Leu Ser Arg Pro Trp Trp Met Cys Ser Arg Arg Gly Lys Asp Ile Ser
                215                220                225

tgg aac ttc tgacagaggt gacccggcgg atggcagaag cagagctggt 778
Trp Asn Phe
    230

tcaagaagga aaagcaagga aaacgaaccc tgaaatccaa agcaccctcc ggaaacggct 838

gtatctgcag tag 851
    
```

*Fig. 8B*

aggatcagac aagggtgctg agagccggga ctcacaacca aaggagaa atg agc aat 57  
 Met Ser Asn  
 1

ccg cgg tct ttg gaa gag gag aaa tat gat atg tca ggt gcc cgc ctg 105  
 Pro Arg Ser Leu Glu Glu Glu Lys Tyr Asp Met Ser Gly Ala Arg Leu  
 5 10 15

gcc cta ata ctg tgt gtc acc aaa gcc cgg gaa ggt tcc gaa gaa gaa 153  
 Ala Leu Ile Leu Cys Val Thr Lys Ala Arg Glu Gly Ser Glu Glu Glu  
 20 25 30 35

gag ctg gaa aaa ttc cag cag gcc atc gat tcc cgg gaa gat ccc gtc 201  
 Glu Leu Glu Lys Phe Gln Gln Ala Ile Asp Ser Arg Glu Asp Pro Val  
 40 45 50

agt tgt gcc ttc gtg gta ctc atg gct cac ggg agg gaa ggc ttc ctc 249  
 Ser Cys Ala Phe Val Val Leu Met Ala His Gly Arg Glu Gly Phe Leu  
 55 60 65

aag gga gaa gat ggg gag atg gtc aag ctg gag aat ctc ttc gag gcc 297  
 Lys Gly Glu Asp Gly Glu Met Val Lys Leu Glu Asn Leu Phe Glu Ala  
 70 75 80

ctg aac aac aag aac tgc cag gcc ctg cga gct aag ccc aag gtg tac 345  
 Leu Asn Asn Lys Asn Cys Gln Ala Leu Arg Ala Lys Pro Lys Val Tyr  
 85 90 95

atc ata cag gcc tgt cga gga gaa caa agg gac ccc ggt gaa aca gta 393  
 Ile Ile Gln Ala Cys Arg Gly Glu Gln Arg Asp Pro Gly Glu Thr Val  
 100 105 110 115

ggt gga gat gag att gtg atg gtc atc aaa gac agc cca caa acc atc 441  
 Gly Gly Asp Glu Ile Val Met Val Ile Lys Asp Ser Pro Gln Thr Ile  
 120 125 130

cca aca tac aca gat gcc ttg cac gtt tat tcc acg gta gag gga tac 489  
 Pro Thr Tyr Thr Asp Ala Leu His Val Tyr Ser Thr Val Glu Gly Tyr  
 135 140 145

atc gcc tac cga cat gat cag aaa ggc tca tgc ttt atc cag acc ctg 537  
 Ile Ala Tyr Arg His Asp Gln Lys Gly Ser Cys Phe Ile Gln Thr Leu  
 150 155 160

*Fig. 9A*

gtg gat gtg ttc acg aag agg aaa gga cat atc ttg gaa ctt ctg aca 585  
Val Asp Val Phe Thr Lys Arg Lys Gly His Ile Leu Glu Leu Leu Thr  
165 170 175

gag gtg acc cgg cgg atg gca gaa gca gag ctg gtt caa gaa gga aaa 633  
Glu Val Thr Arg Arg Met Ala Glu Ala Glu Leu Val Gln Glu Gly Lys  
180 185 190 195

gca agg aaa acg aac cct gaa atc caa agc acc ctc cgg aaa cgg ctg 681  
Ala Arg Lys Thr Asn Pro Glu Ile Gln Ser Thr Leu Arg Lys Arg Leu  
200 205 210

tat ctg cag tag 693  
Tyr Leu Gln

*Fig. 9B*

1 MESEMSDPQLQEERYDMSGARLALTLCVTKAREGSEVDMEALERMFRL 50  
|||. |::|:||||||||| ||||||||| |::||| ||| |  
1 ....MSNPRSLEEEKYDMSGARLALTLCVTKAREGSEEDLDALEHMFRL 46  
51 KFESTMKRDPTAQFLEELDEFQQTIDNWEVPVSFAFVVLMAHGEEGLLK 100  
:|||||||||:| |||:| || |::|:||||||||| || ||  
47 RFESTMKRDPTAEQFQEELEKFQQAIDSREDPVSCAFVVLMAHGREGFLK 96  
101 GEDEKMRLEDLFEVLNNKNCKALRGKPKVYIIQACRGEHRDPGEELRGN 150  
||| |::|:| || |||||:| ||||||||||| ||| |  
97 GEDGEMVKLENLFEALNNKNQALRAKPKVYIIQACRGEQRDPG..... 140  
151 EELGGDEELGGDEVAVLKNPQSIPTYTDTLHIYSTVEGYLSYRHDEKGS 200  
| .||| | |::|..|:||||| |::|:|||||: |||:| ||  
141 ETVGGDE.....IVMVIKDSPTIPTYTDALHVYSTVEGYIAYRHDQKGS 185  
201 GFIQTLTDVFIHKKGSILELTEEITRLMANTEVMQEGKPRKVNPEVQSTL 250  
||||| ||| :|| |||| |::| || |..||| || |||:||||  
186 CFIQTLVDVFTKRKGHILELLTEVTRRMAEELVQEGKARKTNPEIQSTL 235  
251 RKKLYLQ\* 257  
||:||||  
236 RKRLYLQ\* 242

*Fig. 10*